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GenCore version 5.1.3
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February 16, 2003, 15:50:54 ; Search time 2481.53 Seconds
 (without alignments)
 16465.781 Million cell updates/sec 1 atgaagaacaacatcctggt......tgatctcttactacctgctg 1404 4109280 2054640 segs, 14551402878 residues Total number of hits satisfying chosen parameters: - nucleic search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-09-497-967-5 GenEmbl:* Title: Perfect score: Sequence: Scoring table: OM nucleic Database : Searched: Run on:

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em_htgo_mus:*
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em_htg_other:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AF324424 100 3026 bp DNA linear INV 27-FEB-2002 Ichthyophthirius multifilis immobilization antigen isoform ichthyophthirius multifillis. Ichthyophthirius multifillis Bukaryota; Alveolata; Cillophora; Oligohymenophorea; Bymenostomatida; Ophryoglenina; Ichthyophthirius. 1 (bases I to 3026) Lin.Y., Lin,T.L., Wang,C.C., Wang,X., Stieger,K., Klopfleisch,R. AF324424.1 GI:12698726 RESULT 1
AF324424
LOCUS
DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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variation in primary sequence and tandem repeat i-antigens of Ichthyophthirius multifillis Mol. Biochem. Parasitol. 120 (1), 93-106 (2002) 21839613
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Pred. No. 8.3e-218;
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                                                                     Lin,Y., Lin,T.-L. and Clark,T.G.
Lin,Y., Lin,T.-L. and Clark,T.G.
Direct Submission
Submitted (27-NOV-2000) Microbiology
University, Ithaca, NY 14853, USA
Location/Qualifiers
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Best Local Similarity 72.5%;
Matches 1013; Conservative
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Clark, T.G., Lin, T.-L., Jackwood, D.A. and Dickerson, H.W.
Direct Submission
Submitted (29-MAR-1999) Microbiology & Immunology, Cornell
University, College of Veterinary Medicine, Ithaca, NY 14853, USA
                                                                                       ichthyophthirius multifiliis.
Ichthyophthirius multifiliis.
Eukaryote, Alveolate, Ciliophora; Oligohymenophorea;
Eukaryote, Alveolate, Ciliophora; Oligohymenophorea;
Hymenostcmatida; Ophryoglenina; Ichthyophthirius.

1 (bases 1 to 2486)
Lark, T.G., Lin, T.L., Jackwood, D.A., Sherrill, J., Lin, Y. and
Dickerson, H.W.
The gene for an abundant parasite coat protein predicts tandemly
Gene 229 (1-2), 91-100 (1999)
                                                                                                                                                                                                                                                                                                                    (pases 1 to 2486)
Gaertig,J., Gao,Y., Tishgarten,T., Clark,T.G. and Dickerson,H.W.
Surface display of a parasite antigen in the ciliate Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1098 TACCGCTGGAGGAACCGCTACCCTGATCGCTCAGTGTCTCTGGAGTGTCCTGCTGGAAC 1157
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Ichthyophthirius multifiliis immobilization antigen precursor
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310 c 321 q 959 t
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399. .1845
                 (IAG48) gene, complete cds.
AF140273
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                                                         AF140273.1 GI:4868370
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/gene="IAG48"
493. .1758
/gene="IAG48"
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HGPEVLGVYTWBSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
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/gene="JPH3"
/note="component of the junctional complex between plasma
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission (05-007-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA 1. 125020
                                    1563 TICTGCTGCTTTTTTTGCATCAAAACAACTGGTTTTACAGCAGGTACTGATACATGTAC 1622
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1218 TGCTGCTAACTTCTACACCACCAAGCAGACGGACTGGGTGGCTGGAATCGACACCTGTAC 1277
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Manmalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H. Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., A repeat expansion in the gene encoding junctophilin-3 is associated with Buntington disease-like 2
21583737
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                                                                        /map="16q24_3; between D16s520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
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/rpt_unit=ctg
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/gene="JPH3"
/note="JPH3"
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a 32731 c 30696 g 28283 t
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AF429315
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/protein_id="AAL40941.1"
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/chromosome="16"
                                                                                                                                                                              1683 AAAAGTATAATGCCCCTCCACTACTTTC 1710
                                                                                                                                                  1338 GAACATCCAGTGTGACTTCGCTAACTTC 1365
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199 ACCCCTTGTCCTCAGAAGAAGGACGCTGGAGCTCAGCCTAACCCTCCTGCTACCGCTAAC
                                                                      GCTCCTAACTTCAACGCTGGAGCTTCTACCTGTACCGCTTGTCCTGTGAACCGCGTGGGA
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SISGCTFCKVDFXFNGGNPAAQCGTECPAGTLYTDGVTPTTYTYSLSQCVNCRAGFYQNS
NFEAGKSGCNKCAVSKTGSASVPGNSATSATQCOUNDCPAGTVUDGTSTNFVALASEC
TKCQANPYASKTSGFAAGTDTCTECSKKLTSGATAKVYAEATQKAQCASSTFAKFLSM
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/product="52kDa immobilization antigen variant B protein"
/protein_id="AAK94941.1"
Ichthyophthirius multifillis 52kDa immobilization antigen variant protein mRNA, complete cds. AF405431
                                                                                                                                                                                                                                              Variation in primary sequence and tandem repeat copy number among i-antigens of Ichthyophthirius multifillis
Mol. Blochem. Parasitol. 120 (1), 93-106 (2002)
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                                                                                                                     ichthyophthirius multifiliis.
Eukaryota, Alveolata; Ciliophora; Oligohymenophorea;
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 1520)
Lin, Y., Lin, T.L., Wang, C.C., Wang, X., Stieger, K., Klopfleisch, R. and Clark T.G.
and Clark T.G.
Variation in primary sequence and tandem repeat copy number amonty.
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Pred. No. 0.00021;
0; Mismatches 136; Indels 9

    1. 1220
    /organism="Ichthyophthirius multifiliis"

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Lin,Y., Wang,J.C. and Clark,T.C.
Direct Submission
Submitted (03-AUG-2001) Microbiology of
University, Ithaca, NY 14853, USA
Location/Qualifiers
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/note="IAG52B[G5]"
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RESULT 5

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Query Match 3.7°
Best Local Similarity 52.5
Matches 114; Conservative
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TAGAQANLATQCSNQCPTGTYLDDGYTLVFNTSATLCVKCRPNFXNGSPQGEAPGY
QVFAAGAAAAGVAAYTSQCVPCQINKNDSPATAGAQANLATQCSTQCPTGTAIQDGYT
LVFSNSSTQCSQCTANYFFNGNLEAGKSQCLKCPVSKTTPAHAPGNNATQATQCLTTC
PAGTVLDDGTSTNFVASATECTKCSAGFFASKTTGFTAGTDTCTECTKKLTSGATAVN
                     1249\ bp mRNA linear INV 18-SEP-1998 multifilis immobilization antigen precursor,
                                                                                                                                                                                                                                                                                                 Clark, T.G., McGraw, R.A. and Dickerson, H.W.
Clark, T.G., McGraw, R.A. and Dickerson, H.W.
Developmental expression of surface antigen genes in the parasitic
cliate Ichthyophthirius multifillis
Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-SEP-1998) Microbiology and Immunology, Cornell University, Ithaca, NY 14853, USA Sequence update by submitter on Sep 18, 1998 this sequence version replaced gi:159289.
                                                                                                                                  Ichthyophthirius mutifillis.
Eukaryota: Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 1249)
Lin, T.L. and Dickerson, H.W.
Purification and partial characterization of immobilization J. Protozool. 39 (4), 457-463 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (06-JUN-1992) Microbiology and Immunology, Cornell
University, Ithaca, NY 14853, USA
4 (bases 1 to 1249)
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/product="immobilization antigen"
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177. .893
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                                                                                                                    Ichthyophthirius multifiliis
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243 c 257 g
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/citation=[1]
/codon_start=3
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                                   Ichthyophthirius multimRNA, partial cds.
M92907
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                   ICYIMANT
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1. Solutions 1 to 125020)

1. Solutions 1 to 125020)

1. Solutions 2. E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submitseaton

1. Submitted (05-07-2001) Psychiatry, Johns Hopkins Medical

1. Submitted (05-07-2001) Psychiatry, Johns Hopkins Medical

1. Solutions, 600 N. Wolfe St., Baltimore, MD 21287, USA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125020)

Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Pingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 is Nat. Genet. 29 (4), 377-378 (2001)
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                                                                                                                                                                                                                                  1016 AGTACTTGATGATGAACATCAACTAATTTTGTAGCTTCCGCAACTGAATGTACTAAATG 1075
                                                                                                                                                                       1098 TACCGCTGGAGGAACCGCTACCCTGATCGCTCAGTGTCTCTGGAGTGTCCTGCTGGAAC 1157
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                        Length 1249;
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AF429315.1 GI:17646244
                                                                                                            Indels
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Score 52.2; DB 3;
Pred. No. 0.00089;
0; Mismatches 103;
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/rpt_unit=ctg
complement(<36507. .>36887)
/gene="JPH3"
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complement(<36507. 36887)
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/protein_id="AAL40941.1"
/db_xref="GI:17646245"
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Consensus quality: 217356 bases at least Q40
Consensus quality: 223517 bases at least Q30
Consensus quality: 2243517 bases at least Q30
Consensus quality: 224119 bases at least Q20
Consensus quality: 224119 bases at least Q20
Estimated insert size: 258000; agarose-fp estimation
Estimated insert size: 228572; sum-of-contigs estimation
Quality coverage: 7.65 in Q20 bases; agarose-fp estimation
Quality coverage: 8.64 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence it currently
* NOTE: This is a 'working draft' sequence record is
* arbitrary. Gaps between the configs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved. AC073693 230372 bp DNA linear HTG 29-JUN-2000 MUS musculus clone RP23-152L22, WORKING DRAFT SEQUENCE, 19 Direct Submission Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Mus. of 14664 bp in length unknown length of 18065 bp in length 10024 bp in length unknown length of 8689 bp in length unknown length of 1528 kp in length unknown length unknown length of 9596 bp in length contig of 1343 bp in length gap of unknown length unknown length of 5714 bp in length unknown length of 2215 bp in length in length of 2104 bp in length 8079 bp in length bp in length length unknown length length length length length of 11632 bp 2409 bp contig of 1087 b gap of unknown 1 contig of 1528 b gap of unknown 1 unknown unknown unknown unknown unknown Center Project Name: 1795526 Center clone name: RPCI-23_152L22 Web site: http://www.jgi.doe.gov oţ of of -----Genome Center Center: Joint Genome Institute Center Code: JGI Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 230372) DOE Joint Genome Institute. contig gap of contig gap of gap of contig gap of contig contig contig gap of contig contig contig gap of oĘ gap of HTG; HTGS_PHASE1; HTGS_DRAFT. gap of dap of 2 (bases 1 to 230372) DOE Joint Genome Institute. gap 80384: 98449: AC073693.1 GI:8810310 34975: 43664: 53888: 34875: 1087: 2715: 2815: 11186: 7100: Sequencing of Mouse Project Information unordered pieces Mus musculus. Mus musculus 111187 11287 17001 17101 25280 34876 34876 43765 53789 65521 65621 80285 80385 4159 4259 6474 6574 8983 Unpublished 2816 AC073693

Louis

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Waters.cu., Cubmission
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
Onlyersity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Onlyersity, 2001 this sequence version replaced gi:15887350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is RP11-549C16, 2000 bp overlap; the clone sequenced to the right is RP11-115D19. Actual start of this clone is at base position 123633 of RP11-549C16; actual end is at base position 159764 of RP11-582C12.
                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACC3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence derived from one plasmid subclone, base position 55515
                       University School of Medicine, 4444 Forest Park Parkway, St. MO 53108, USA
6 ( bases 1 to 159764)
Waterston, R.
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Location/Qualifiers
                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WGSC WGSC Web site: http://genome.wustl.edu/gsc Contact: saplens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                 Center project name: H_NH0582C12
Drafting Center: WIBR
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/db_xref="taxon:9606"
/chromosome="4"
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137. ,299
/rpt_family="ERV1"
302. ,653
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/rpt_family="ERV1"
646. .735
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/rpt_family="ERV1"
811. .1176
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159764)
Sulston, J. E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 GCTGCTGTTTGGTGCCTGGAGCTTCTACCTGTACCCTTGTCCTCAGAAGAAGGACGCT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 GGAGCTCAGCCTAACCCTCCTGCTACCGCTAACCTGGTGACCCAGTGTAACGTGAAGTGT 285
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  9859 98549: gap of unknown length 16262: contig of 17713 bp in length 16362: gap of unknown length 16363: ld6362: gap of unknown length 17707 140806: contig of 24344 bp in length 17707 167609: contig of 26803 bp in length 1710 19938: contig of 26803 bp in length 1710 19938: contig of 31689 bp in length 1799 199498: gap of unknown length 1899 230372: contig of 30874 bp in length 160cation/Qualifiers
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53740 c 52522 g 61042 t 1802 others
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Pearman, C., Meyer, R. and Doebber, A.
The sequence of Homo sapiens BAC clone RP11-582C12
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53.9%; Pred. No. 0.51
tive 0; Mismatches
                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-152L22"
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3 (bases 1 to 159764)
Waterston, R.H.
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Waterston, R.H.
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Waterston, R.H.
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12816. 13318
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13323. 13373. 13373
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1 (bases 1 to 643)
Armbrust, E.V. and Galindo, H.M.
Rapid evolution of a sexual reproduction gene in centric diatoms of the genus Thalassiosira
Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
21365169
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2 (bases 1 to 643)
Armbrust, E.V. and Galindo, H.G.
Armbrust, E.V. and Galindo, H.G.
Submission
Submission
Submitted (27-APR-2001) Oceanography, University of Washington, Box Submittels, WA 98195-7940, USA
357940, Scattle, WA 98195-7940, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 bp DNA linear PLN 27-JUL-2001
Thalassiosira weissflogii isolate CCMP 1336 clone 10 sexually
induced protein SIG 1 gene, partial cds.
AP374493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 133672 GAAGCCTTCAGAGAGATGGGGTGACTGGTCTCTGGGTGCCCAGCGATAAGGGGGTTCACAGA 133731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 133732 GTAAAGGACATCTACTACAACCATGTTCTTGGGAGCTATAAACTAGGAAGTGAACC 133791
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Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GAGACCAACACCGCTGGACAGGTGGACGACCTGGGAACCCCTGCTAACTGTGTGAACTGT 141
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/isolate="CCMP 1336"
/db_xref="taxon:67004"
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24311. 24706
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/rpt_family="AT_rich"
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/rpt_family="L1"
24833. .24881
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1 (bases 1 to 179217)

8 Akhter, N. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakseley, K.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Lee-Lin, S.O., Legaspl.R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., NISC Comparative Sequencing Initiative
Innovaliative Sequencing Initiative
                                                        /translation="SERMCTCDRNFOGADCSLRTCPFGKAHVDTPRGDLDASLTIGDH NDIILAGSTLYPYGITEGFPLMSDTAGTVIANTAHDYMECSNKGLCDRINVLCECPPG YDGAACQRASCPSKANSSTPGSGOGERSNTNFKVFNANSAFHGRAAEVVQRDQCSGHG TCWTIEQLAEDHGNTYDLWBKDVYM"

163 c 144 q 170 t
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Bos taurus clone RP42-504H16, WORKING DRAFT SEQUENCE, 5 ordered
                                                                                                                                                                                                                                                                        278 TGAAGTGTCCTGCTGGAACCGCTATCGCTGGAGGAGCTACCGACTACGCTGCTATCATCA 337
                                                                                                                                                                                                                                                                                               338 CCGAGTGTGTGAACTGTCGCATCAACTTCTACAACGAAACGCTCCTAACTTCAACGTG 397
                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 179217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (15-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 15, 2002 this sequence Version replaced gi:17017552.
                                                                                                                                                                                                                                                 ;
/product="sexually induced protein SIG 1"
/protein_id="AAK61135.1"
/db_xref="GI:14336350"
                                                                                                                                                                                                       8; Length 643;
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Pred. No. 1.6;
0; Mismatches
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HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                            144 9
                                                                                                                                                                                                                                                                                                                                                                                                                                 398 GAGCTTCTACCTGTACCGCTTGTCC 422
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Matches 80; Conservative
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The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contigh has been established using one or more of the following: read-pair clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in QSD bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 32314: contig of 32314 bp in length
                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177994 bases at least Q40
Consensus quality: 178672 bases at least Q30
Insert size: 136000; agarose-fp
Insert size: 136000; agarose-fp
Insert size: 178817; sum-of-contigs
Quality coverage: 12.94x in Q20 bases; agarose-fp
Quality coverage: 12.94x in Q20 bases; sum-of-contigs
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/note="clone overlaps with GenBank Accession Number
AC113228 clone RP42-67B23 (center project name crl)"
1 38501 c 36655 g 49899 t 400 others
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66236: gap of unknown length
80633: contig of 14397 bp in length
80733: gap of unknown length
92700: contig of 11967 bp in length
92800: gap of unknown length
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Best Local Similarity 50.2%; Pred. No. 2.5;
Matches 101; Conservative 0; Mismatches 100; Indels
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/note="assembly_fragment"
66237. .80633
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/note="assembly_fragment"
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/db_xref="taxon:9913"
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164910. .179217
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vector_side:left"
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1. .32314
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843 TACCTGTCTGCCTTGTCCTGCTAACAAGGACTACGGAGCTGAGGCTACCGCTGGAGGAGC 902

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Contact: nisc_zoo@nhgrt.nih.gov ------ Project Information Center project name: crq Center clone name: 504H16

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/www.neal- ul:14330348"
/translation="SHDMCTCDRNFQGADCSLRTCPFGKAHVDTPRGDLDASLTIGDH
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TCMTIEQLAFLDHYYDLWNDVTW
                                                                                                                                                                                                                                          1 (bases 1 to 643)
Armbrust, E.V. and Galindo, H.M.
Rapid evolution of a sexual reproduction gene in centric diatoms of the genus Thalassiosira
Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
                                                                                   AF374492 643 bp DNA linear PLN 27-JUL-2001
Thalassiosira weissflogii isolate CCMP 1336 clone 9 sexually
induced protein SIG 1 gene, partial cds.
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Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
Thalassiosira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 CCTGTACCCCTTGTCCTCAGAAGAAGGACGCTGGAGCTCAGCCTAACCCTCCTGCTACCG 253
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Armbrust, E.V. and Galindo, H.G.
Bubrect Submission
Submitted (27-78R-2001) Oceanography, University of 357940, Seattle, WA 98195-7940, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAACGCTCCTAACTTCAACGCTGGAGCTTCTACCTGTACCGCTTGTCC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /country="USA: Long Island, NY"
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join(<1. 56,141. >643)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="sexually induced protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 38.6; DB 8;
48.0%; Pred. No. 8.2;
iive 0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:67004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
CAGCTTGCCAGCGTGCATCATGTCC 342
                                                                                                                                                                                        Thalassiosira weissflogil.
Thalassiosira weissflogil
                                                                                                                                                          AF374492.1 GI:14336347
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Matches 11
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HSCOLPDGF/c
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SOURCE
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                    318
                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                RESULT 12
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                                                                                                                                                                                                                                                                               Thalassiosira weissflogii isolate CCMP 1336 clone 13 sexually induced protein SIG 1 mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        centric diatoms of
                                                                                                                                     DD 106790 CICCCCCATCCTGGGATTCTCCAGGCAAGAACACTGGAGTGGGTTGCCATTTCCTTCTC 106849
      Thalassiosira weissflogii.
Thalassiosira weissflogii
Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 TGAAGIGTCCTGCTGGAACCGCTATCGCTGGAGGAGCTACCGACTACGCTGCTATCATCA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 CCGAGTGTGTGAACTGTCGCATCAACTTCTACAACGAGAACGCTCCTAACTTCAACGCTG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 ATAAGGGATTATGCGATCGCATCAATGCCCTTTGCGAATGTCTTCCTGGCTATGACGGTG 317
                                                                                                                   963 AGCTACCAACTACGTGATCCTGCAGACCGAGTGTCTGAACTGTGCTGAACTTCTACTT 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (pases 1 to 591)
Armbrust, E.V. and Galindo, H.M.
Rapid evolution of a sexual reproduction gene in cetthe quant Thalassiosira
Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Thalassiosira weissflogii"
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                                                                                                                                                                                                                       Db 106850 CAATGCATGAAAGTGAAAAGC 106870
                                                                                                                                                                                        1023 CGACGGAAACAACTTCCAGGC 1043
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Matches 79; Conservative
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ORIGIN
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AUTHORS
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TITLE
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AF374552
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Washington, Box

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Gaps

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Indels

Length 643;

SIG 1"

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11564. .11617,12068. .12112,12206. .12304,12602. .12709,
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4764. 4865,5588. 5659,5887. 5931,6090. 6143,6366. 6359,
6858. 6911,7028. 7081,7421. 7474,7563. 7607,7724. 7777,
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7geng...Collal.
                                                                                                                                                            EUKaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (basea I to 16814)
Slimon, M. P., Pedeutour, F., Sirvent, N., Grosgeorge, J., Minoletti, F., Colndre, J.M., Terrier-Lacombe, M.J., Mandahl, N., Craver, R.D., Fransson, I., Guilbaud, C. and Dumanski, J.P., Kedra, D., Fransson, I., Guilbaud, C. and Dumanski, J.P., Redra, D., Fransson, I., Guilbaud, C. and Dumanski, J.P., Mandahlin of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans and glant-cell fibroblastoma
Nat. Genet. 15 (1), 95-98 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Join 2603. .2705,4168. .4362,4501. .4535,4638. .4673,
4764. .4815,5588. .5659,5887. .5931,6090. .6143,6306. .6359,
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HSCOLPDGF 16814 bp DNA linear PRI 12-MAR-1997
H.sapiens DNA sequence of COLIA1 gene fused with intron 1 of PDGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-JUN-1996) K.P. O'Brien, Dept. of Molecular Medicine, Cinital Genetics Unit, Karolinska Hospital, Building L-6, S-171 79 Stockholm, SWEDEN 103559, M10627, X07884, M20789 and K01228. Location/Qualifiers
                                                                 X98705.1 GI:1888408
COLJA1 gene; collagen alpha 1 type I; PDGFB gene; platelet-derived
growth factor beta; translocation breakpoint.
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O'Brien, K.P.
Direct Submission
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Nostoc sp. PCC 7120 plasmid pCC7120alpha DNA, complete genome,
section 1/2.
Ap003600 BA000020
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8388 GGAAACCCAACCTTGCCTCTCGGGATGGCAGGAGGAAGGGGAGACAGGGACAGGAGAAGAGA 8329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research Submitted. The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:kaneko@kazusa.or.jp, UKL:http://www.kazusa.or.jp/cyanobase/, Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120 DNA Res. 8 (5), 205-213 (2001) 21595285 2 (bases 1 to 341950)
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ive 0; Mismatches 189; Indels
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Quality: Phrap Quality >=40 99.3% of Sequence;
Estimated Total Number of Errors is 0.9.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 223kb). It is clipped at the overlap with AC009002. The
number of bases overlapped is 5260.
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Homo sapiens chromosome 19 clone CTD-2639E6, complete sequence.
AC026803
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Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Genome Institute, 24271)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (16-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 16, 2002 this sequence version replaced gi:21637469.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Submission Submission Submission Old-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 224271) DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 224271)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Gaps
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Finishing Completed at Stanford Human Genome Center
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2.7%; Score 38.4; DB 9;
Best Local Similarity 49.5%; Pred. No. 15;
Matches 99; Conservative 0; Mismatches 101;
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